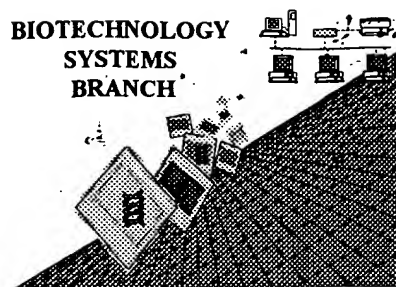


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/701,618
Source: P4/09
Date Processed by STIC: 8/1/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Sample of submitted file

09/701,618 I

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: *7 more up - all responses must be* Does Not Comply
~~(A) NAME: Deutsches Krebsforschungszentrum~~ on Corrected Diskette Needed
~~(B) ROAD: Im Neuenheimer Feld 280~~ *same line as heading*
delete ~~(C) PLACE: Heidelberg~~
~~(E) COUNTRY: Deutschland~~
~~(F) POSTAL CODE: 69120~~

(ii) TITLE OF THE INVENTION: Method for Triggering Apoptosis In Cells

(iii) NUMBER OF SEQUENCES : 10

(v) ~~FOR~~ COMPUTER-READABLE VERSION: *MEDIUM TYPE:*

- (A) ~~DATA CARRIER:~~ Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(vi) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE:
(B) STREET:
(C) CITY:
(D) STATE:
(E) COUNTRY:
(F) ZIP:

Insert these mandatory headings and responses for a U.S. case

(vi) ~~FOR~~ CURRENT APPLICATION DATA:
DATA OF THE PRESENT INVENTION:

not yet known
~~SEQUENCE IDENTIFICATION DATA:~~
(A) APPLICATION NUMBER:
(B) FILING DATE:

(vii) ~~FOR~~ DATA OF THE PRIORITY APPLICATION:

(A) APPLICATION NUMBER: DE 198 24 811.3

PRIOR APPLICATION DATA: (B) FILING DATE: 3-JUN-1998

INFORMATION FOR SEQ ID NO: 1

(2) ~~STATEMENT TO SEQ ID NO: 1:~~

(i) SEQUENCE CHARACTERISTIC ~~MARK:~~

(A) LENGTH: 1156 pairs of base

TYPE? (B) ~~KIND:~~ Nucleotide nucleic acid

(C) ~~STRANDEDNESS:~~ Einzelstrang

(D) ~~TOPOLOGIE:~~ linear

STRANDEDNESS? *TOPOLOGY*

(ii) ~~KIND OF MOLECULES:~~ cDNA
MOLECULE TYPE:

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

FEATURE
(ix) ~~CHARACTERISTIC:~~

(A) NAME/KEY: CDS

(B) POSITION: 118..540

FEATURE
(ix) ~~CHARACTERISTIC:~~

(A) NAME/KEY: mat_peptide

(B) POSITION: 118..540

SEQUENCE DESCRIPTION:

(xi) ~~DESCRIPTION OF SEQUENCE:~~ SEQ ID NO: 1:

EPO is invalid for a U.S. case

The only acceptable responses

for a U.S. case

are: single, double, both, or unknown

09/10/68

2

(2) ANGABEN ZU SEQ ID NO: 2:

(i) SEQUENZKENNZEICHEN:

(A) L?NGE: 141 Aminos,uren

(B) ART: Aminos,ure

(D) TOPOLOGIE: linear

(ii) ART DES MOLEKŠLS: Protein

(xi) SEQUENZBESCHREIBUNG: SEQ ID NO: 2:

invalid

All sample sequence listings
(attached) for valid format

Also, see sequence header for
valid format

(3) Computer: Apple Macintosh;
 (i) Operating System: Macintosh;
 (ii) Macintosh File Type: text with line termination
 (iii) Line Terminator: Pre-defined by text type file;
 (iv) Pagination: Pre-defined by text type file;
 (v) End-of-file: Pre-defined by text type file;
 (vi) Media: (A) Diskett—3.50 Inch, 400 Kb storage;
 (B) Diskette—3.50 Inch, 800 Kb storage;
 (C) Diskette—3.50 Inch, 1.4 Mb storage;
 (vii) Print Command: Use PRINT command from any Macintosh Application that processes text files, such as MacWrite or Teach Text;
 (4) Magnetic tape: 0.5 Inch, up to 2400 feet;
 (i) Density: 1600 or 6250 bits per Inch, 9 track;
 (ii) Format: raw, unblocked;
 (iii) Line Terminator: ASCII Carriage Return plus optional ASCII Line Feed;
 (iv) Pagination: ASCII Form Feed or Series of Line Terminators;
 (v) Print Command (Unix shell version given here as sample response—mt/dev/rmt0; lpr/dev/rmt0):
 (g) Computer readable forms that are submitted to the Office will not be returned to the applicant.
 (h) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed, a description of the format of the computer readable form as well as the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form and the name and type of computer and operating system which generated the files on the computer readable form. If all of this information cannot be printed on a label affixed to the computer readable form, by reason of size or otherwise, the label shall include the name of the applicant and the title of the invention and a reference number, and the additional information may be provided on a container for the computer readable form with the name of the applicant, the title of the invention, the reference number and the additional information affixed to the container. If the computer readable form is submitted after the date of filing

under 35 U.S.C. 111, after the date of entry in the national stage under 35 U.S.C. 371 or after the time of filing. In the United States Receiving Office, an international application under the PCT, the labels mentioned herein must also include the date of the application and the application number, including series code and serial number.

§ 1.825 Amendments to or replacement of sequence listing and computer readable copy thereof.

(a) Any amendment to the paper copy of the "Sequence Listing" (§ 1.821(c)) must be made by the submission of substitute sheets. Amendments must be accompanied by a statement that indicates support for the amendment in the application, as filed, and a statement that the substitute sheets include no new matter. Such a statement must be a verified statement if made by a person not registered to practice before the Office.

(b) Any amendment to the paper copy of the "Sequence Listing," in accordance with paragraph (a) of this section, must be accompanied by a substitute copy of the computer readable form (§ 1.821(e)) including all previously submitted data with the amendment incorporated therein, accompanied by a statement that the copy in computer readable form is the same as the substitute copy of the "Sequence Listing." Such a statement must be a verified statement if made by a person not registered to practice before the Office.

(c) Any appropriate amendments to the "Sequence Listing" in a patent, e.g., by reason of reissue or certificate of correction, must comply with the requirements of paragraphs (a) and (b) of this section.

(d) If, upon receipt, the computer readable form is found to be damaged or unreadable, applicant must provide, within such time as set by the Commissioner, a substitute copy of the data in computer readable form accompanied by a statement that the substitute data is identical to that originally filed. Such a statement must be a verified statement if made by a person not registered to practice before the Office.

Appendix A—Sample Sequence Listing

(1) GENERAL INFORMATION:

(i) APPLICANT: Doe, Joan X. Doe, John Q
 (ii) TITLE OF INVENTION: Isolation and Characterization of a Gene Encoding a Protease from *Paramecium* sp.
 (iii) NUMBER OF SEQUENCES: 2
 (iv) CORRESPONDENCE ADDRESS:
 (A) ADDRESSEE: Smith and Jones
 (B) STREET: 123 Main Street
 (C) CITY: Smalltown
 (D) STATE: Anystate
 (E) COUNTRY: USA
 (F) ZIP: 12345
 (v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Diskette, 3.50 Inch, 800 Kb storage
 (B) COMPUTER: Apple Macintosh
 (C) OPERATING SYSTEM: Macintosh 5.0
 (D) SOFTWARE: MacWrite
 (vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER: 09/999,999
 (B) FILING DATE: 28-FEB-1989
 (C) CLASSIFICATION: 999/99
 (vii) PRIOR APPLICATION DATA:
 (A) APPLICATION NUMBER: PCT/US88/99999
 (B) FILING DATE: 01-MAR-1988
 (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Smith, John A.
 (B) REGISTRATION NUMBER: 00001
 (C) REFERENCE/DOCKET NUMBER: 01-0001
 (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: (909) 999-0001
 (B) TELEFAX: (909) 999-0002
 (2) INFORMATION FOR SEQ ID NO: 1:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 954 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (iii) HYPOTHETICAL: yes
 (iv) ANTI-SENSE: no
 (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Paramecium* sp.
 (C) INDIVIDUAL/ISOLATE: XYZ2
 (G) CELL TYPE: unicellular organism
 (vii) IMMEDIATE SOURCE:
 (A) LIBRARY: genomic
 (B) CLONE: Para-XYZ2/36
 (x) PUBLICATION INFORMATION:
 (A) AUTHORS: Doe, Joan X. Doe, John Q
 (B) TITLE: Isolation and Characterization of a Gene Encoding a Protease from *Paramecium* sp.
 (C) JOURNAL: Fictional Genes
 (D) VOLUME: 1
 (E) ISSUE: 1
 (F) PAGES: 1-20
 (G) DATE: 02-MAR-1988
 (K) RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 954

BILLING CODE 3510-10-M

ATCGGGATAG	TACTGGTCAA	GACCGGTGGA	CACCGGTAA	CCCCGGTTAA	GTACCGGTTA	60
TAGGCCATTT	CAGGCCAAAT	GTGCCCAACT	ACGCCAATTG	TTTTGCCAAC	GGCCAACGTT	120
ACGTTCGTAC	GCACGTATGT	ACCTAGGTAC	TTACGGACGT	GACTACGGAC	ACTTCCGTAC	180
GTACGTACGT	TTACGTACCC	ATCCCAACGT	AACCACAGTG	TGGTCGCAGT	GTCCCAGTGT	240
ACACAGACTG	CCAGACATTC	TTCACAGACA	CCCC	ATG	ACA	295
				Met	Thr	
				Pro	Pro	
				Glu	Arg	
				Leu		
						-30

TTC CTC CCA AGG GTG TGT GGC ACC ACC CTA CAC CTC CTC CTT CTG GGG 343
Phe Leu Pro Arg Val Cys Gly Thr Thr Leu His Leu Leu Leu Gly
-25 -20 -15

CTG CTG CTG GTT CTG CTG CCT GGG GCC CAT GTGAGGCAGC AGGAGAATGG 393
Leu Leu Leu Val Leu Leu Pro Gly Ala His
-10 -5

GGTGGCTCAG CCAAACCTTG AGCCCTAGAG CCCCCCTCAA CTCTGTTCTC CTAG GGG 450
Gly

CTC ATG CAT CTT GCC CAC AGC AAC CTC AAA CCT GCT GCT CAC CTC ATT 498
Leu Met His Leu Ala His Ser Asn Leu Lys Pro Ala Ala His Leu Ile
1 5 10 15

GTAAACATCC ACCTGACCTC CCAGACATGT CCCCACCAGC TCTCCTCCTA CCCCTGCCTC 558

AGGAACCCAA GCATCCACCC CTCTCCCCCA ACTTCCCCCA CGCTAAAAAA AACAGAGGGA 618

GGCCACTCCT ATGCCTCCCC CTGCCATCCC CCAGGAACTC AGTTGTTTCAG TGCCCACTTC 678

TAC CCC AGC AAG CAG AAC TCA CTG CTC TGG AGA GCA AAC ACG GAC CGT 726
Tyr Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg Ala Asn Thr Asp Arg
20 25 30

GCC TTC CTC CAG GAT GGT TTC TCC TTG AGC AAC AAT TCT CTC CTG GTC 774
Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn Asn Ser Leu Leu Val
35 40 45

TAGAAAAAAT AATTGATTTC AAGACCTTCT CCCCATTCTG CCTCCATTCT GACCATTTC 834

GGGGTCGTCA CCACCTCTCC TTTGGCCATT CCAACAGCTC AAGTCTTCCC TGATCAAGTC 894

ACCGGAGCTT TCAAAGAAGG AATTCTAGGC ATCCCAGGGG ACCCACACCT CCCTGAACCA 954

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(A) NAME/KEY: signal sequence

(B) LOCATION: -34 to -1

(C) IDENTIFICATION METHOD: similarity
to other signal sequences, hydrophobic(D) OTHER INFORMATION: expresses
protease

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Doe, Joan X. Doe, John Q.

(B) TITLE: Isolation and Characterization
of a Gene Encoding a Protease from
Paramecium sp.

(C) JOURNAL: Fictional Genes

(D) VOLUME: 1

(E) ISSUE: 1

(F) PAGES: 1-20

(G) DATE: 02-MAR-1988

(K) RELEVANT RESIDUES IN SEQ ID NO:

2: FROM -34 TO 48

BILLING CODE 2610-10-M

Here's where sequence 2 starts (after
the sequence data of SEQ ID NO: 1:)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Thr Pro Pro Glu Arg Leu Phe Leu Pro Arg Val Cys Gly Thr Thr
-30 -25 -20

Leu His Leu Leu Leu Leu Gly Leu Leu Leu Val Leu Leu Pro Gly Ala
-15 -10 -5

His Gly Leu Met His Leu Ala His Ser Asn Leu Lys Pro Ala Ala His
1 5 10

Leu Ile Tyr Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg Ala Asn Thr
15 20 25 30

Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn Asn Ser Leu
35 40 45

Leu Val

BILLING CODE 3510-16-C